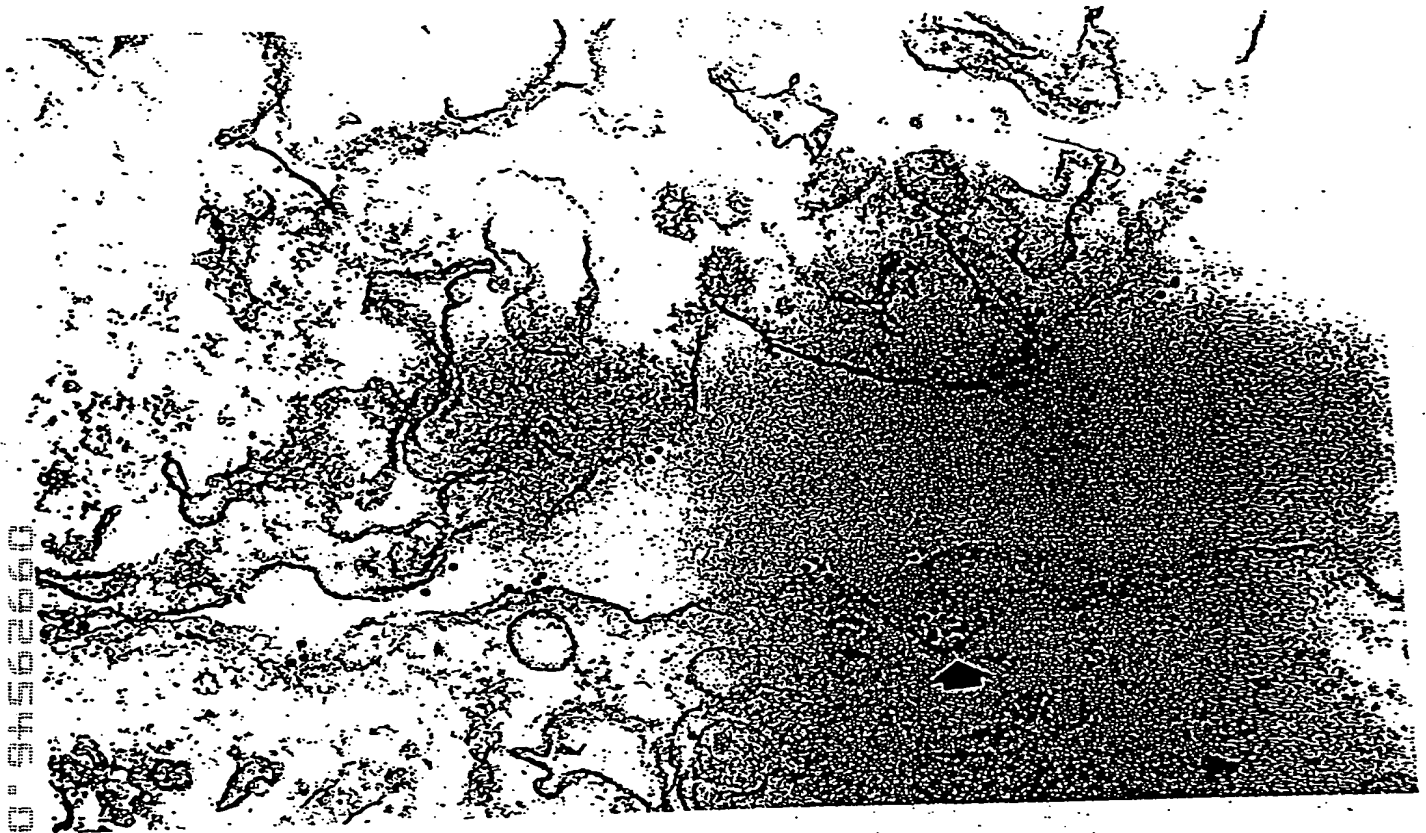


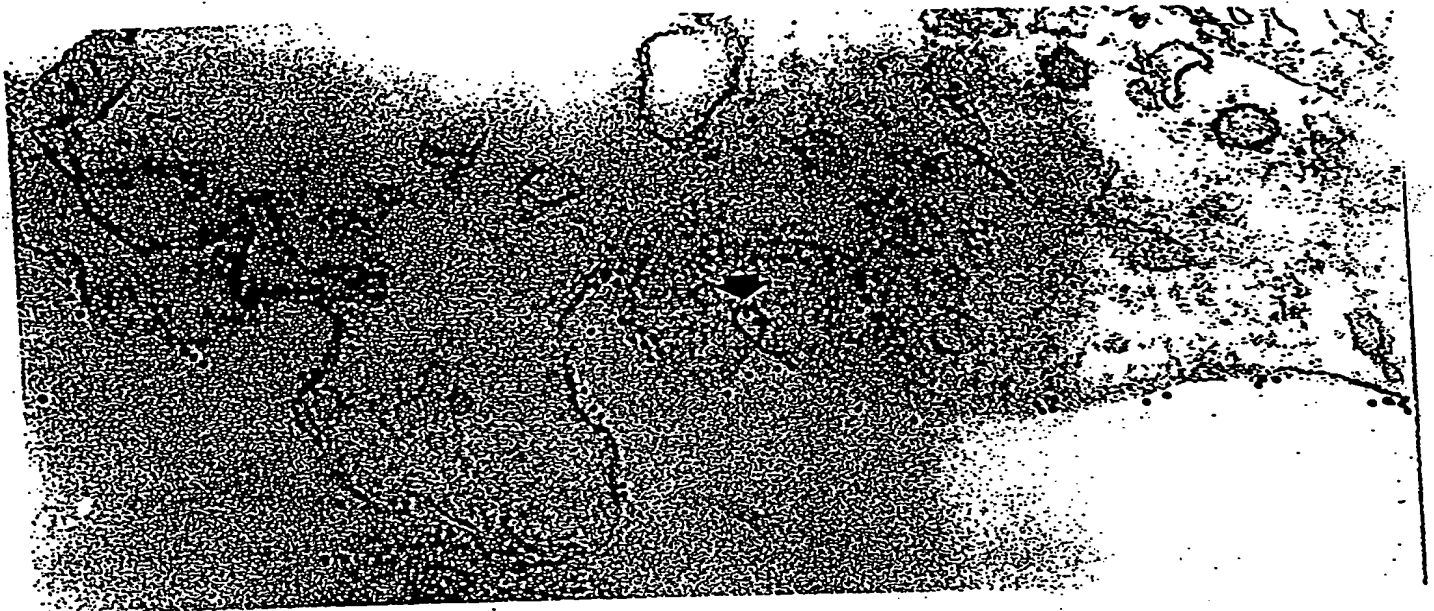
FIGURE 1

**EXPRESS MAIL**  
**EE360933802US**  
**ATTY. DKT. 266/186**  
**SHEET 2 OF 12**



**FIGURE 2**

EXPRESS MAIL  
EL360933802US  
ATTY. DKT. 266/186  
SHEET 3 OF 12



09929546-081304

FIGURE 3

EXPRESS MAIL  
EL360933802US  
ATTY. DKT. 266/186  
SHEET 4 OF 12

Jc879 US PTO

09/929546

08/13/01

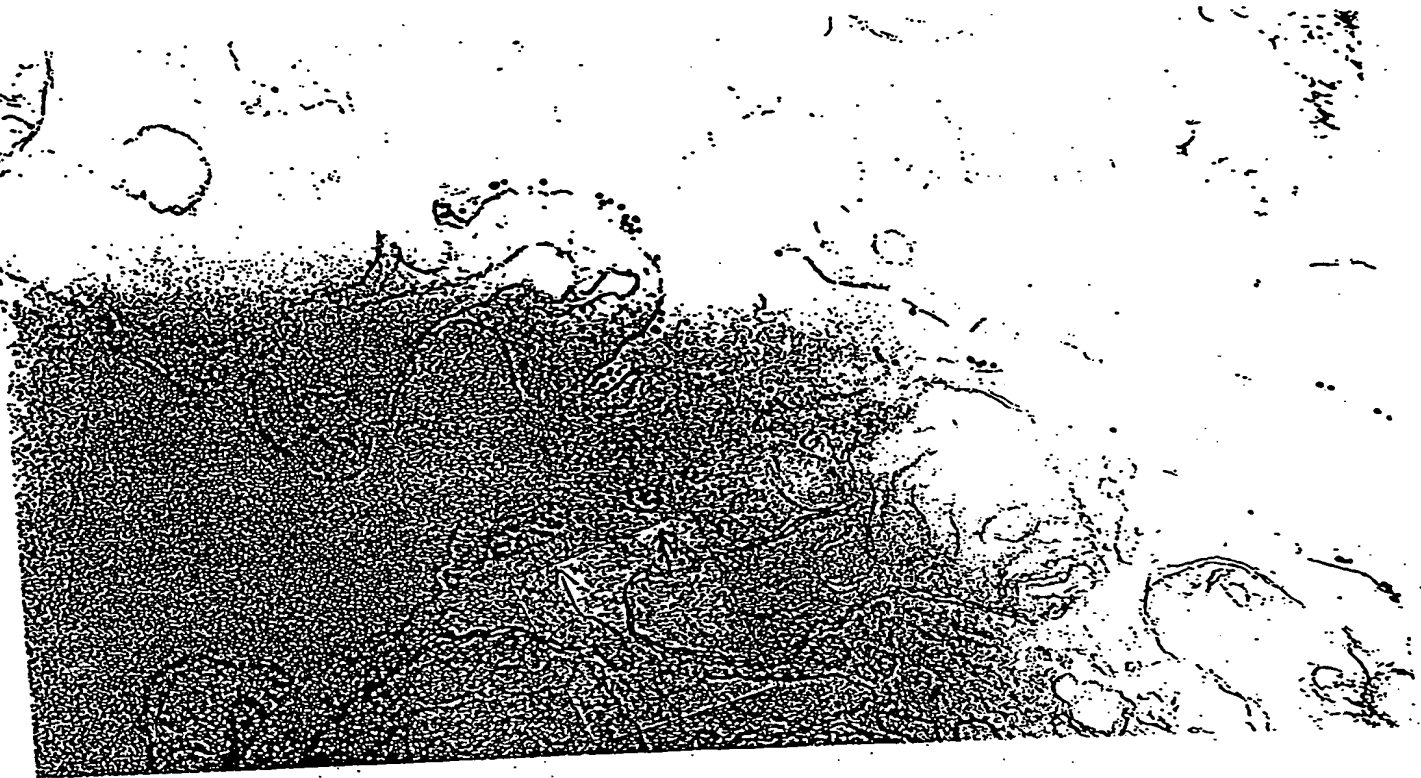


FIGURE 4



FIGURE 5

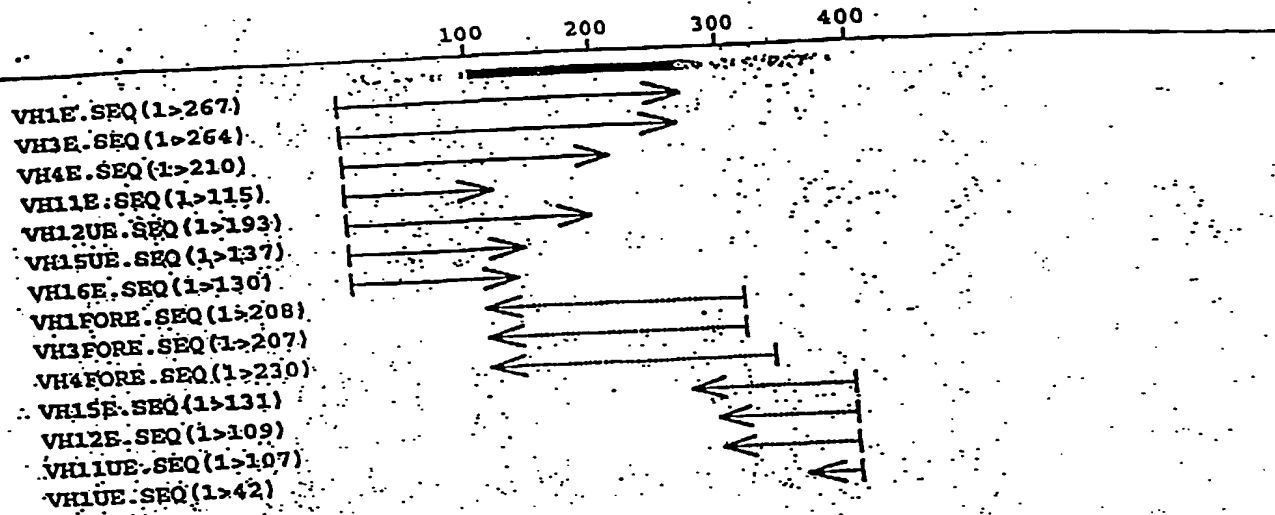


FIGURE 6

Enzymes : All 74 enzymes (No Filter)  
Settings: Linear, Certain Sites Only, Standard Genetic Code

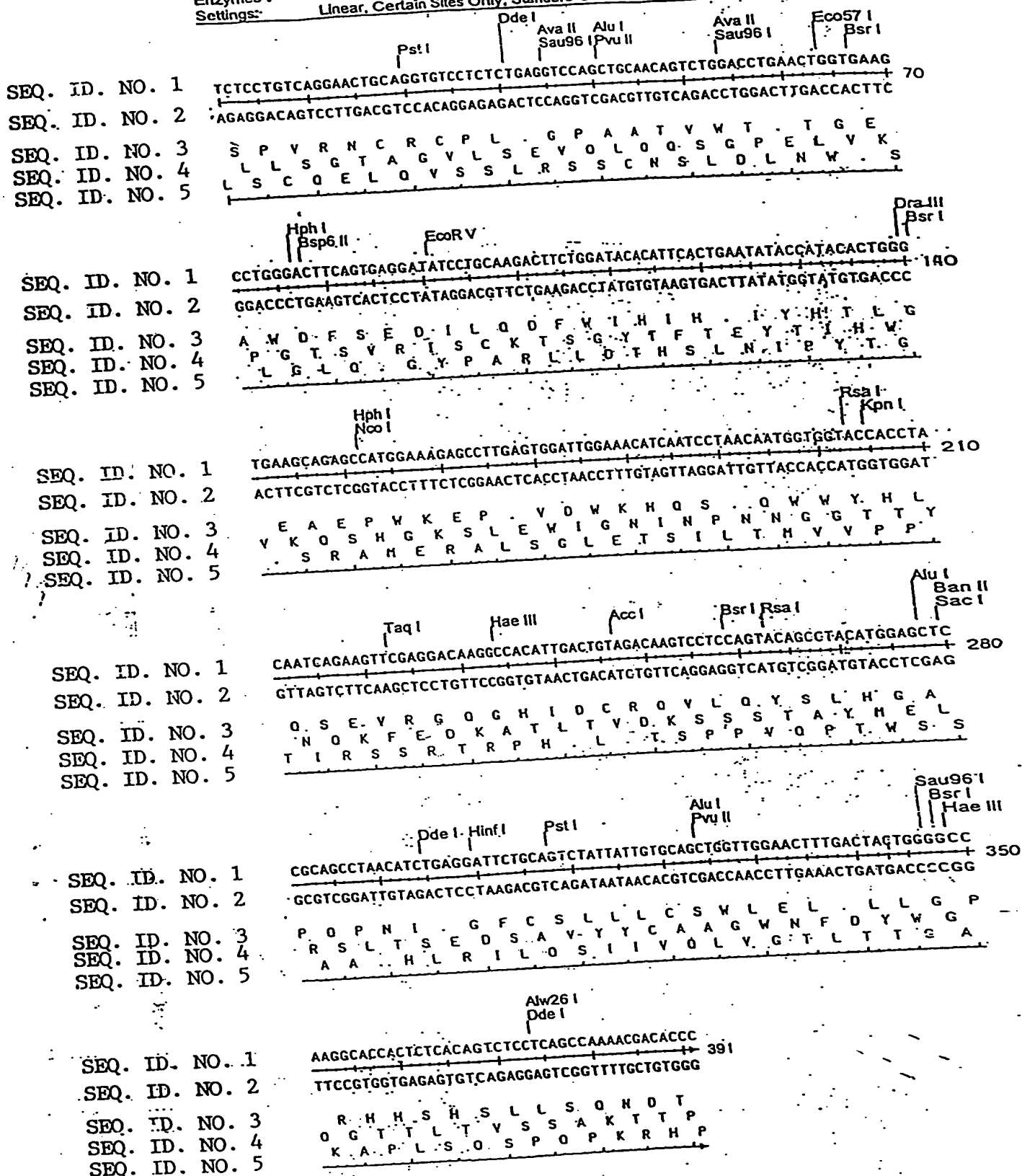


FIGURE 7

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12.

| Seq1(1>115) | Seq2(1>125) | Similarity Index | Gap Number | Gap Length | Consensus Length |
|-------------|-------------|------------------|------------|------------|------------------|
| J591VH.PRO  | MUVHIA.PRO  | 75.6             | 2          | 10         | 125              |
| (1>115)     | (1>125)     |                  |            |            |                  |

```

      10      20      30      40      50
EVQLQQSGPELVKPGTSVRISCKTSGYTFIEYTI-HWVKQSHGKSLEWIGNINPNNGGTT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y::WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNNWVKOSPGKSLEWIGDINPGNGGTS
      10      20      30      40      50      60
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGQGTT
YNQKF:KATLTVDKSSSTAYH:L.SLTSEDSAVYYCA:G.FDYWGQGTT
YNQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGTT
      70      80      90      100      110      120
LTVSS
TVSS
VTSS
  
```

FIGURE 8



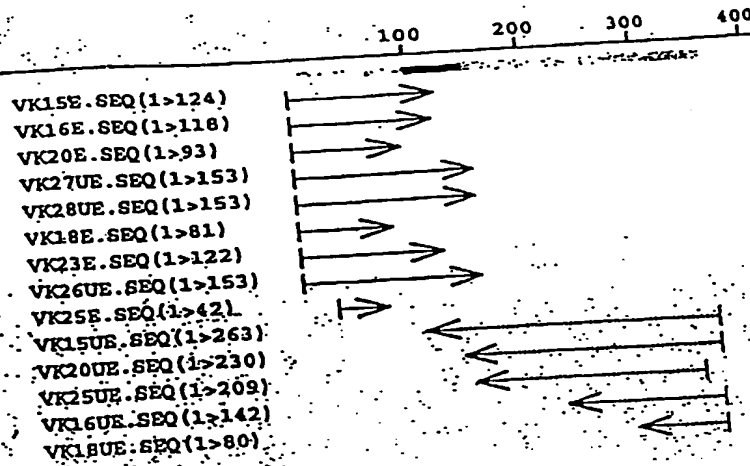


FIGURE 9

Enzymes: All 74 enzymes (No Filter)  
Settings: Linear, Certain Sites Only, Standard Genetic Code

SEQ. ID. NO. 9 TTATATGGAGCTGATGGGAACATTGTAATGACCCAATCTCCCAAATCCATGTCCATGTCAGTAGGAGAGA 70  
SEQ. ID. NO. 10 AATATACCTCGACTACCCCTTGTAACATTACTGGGTTAGAGGGTTAGGTACAGGTACAGTCATCCTCTCT  
SEQ. ID. NO. 11 L Y G A D G N I V H T Q S P K S H S H S V G E  
SEQ. ID. NO. 12 Y H E L H G T L P N L P N P C P C Q E R  
SEQ. ID. NO. 13 I I W S W E H C N D P I S O I H V H V S R R E

SEQ. ID. NO. 9 GGGTCACCTGACCTGCAAGGCCAGTGAGAATGTGGTTAGTTATGTTTCTGGTATCAACAGAAACCAGA 140  
SEQ. ID. NO. 10 CCCAGTGGAAGTGGACGTTCCGGTCACTCTTACACCAATGAATACAAAGGACCATAGTTGTCTTGGTCT  
SEQ. ID. NO. 11 R V T L T C K A S E N V V T Y V S Y Y Q Q K P E  
SEQ. ID. NO. 12 G S P P A R P V R H V L L H F P G I N R N Q  
SEQ. ID. NO. 13 G H L D L Q G Q E C G Y L C F L Y S T E T R

SEQ. ID. NO. 9 GCAGTCTCCTAAACTGCTGATATACGGGGCATCCAACCGGTACACTGGGGTCCCGATCGCTTCACAGGC 210  
SEQ. ID. NO. 10 CGTCAGAGGATTGACGACTATATGCCCGTAGGTTGGCCATGTGACCCAGGGGCTAGCGAAGTGTCCG  
SEQ. ID. NO. 11 Q S P K L L I Y G A S N R Y T G V P D R F T G  
SEQ. ID. NO. 12 S S L L N C Y T G H P T G T L G S P I A S Q A  
SEQ. ID. NO. 13 A V S T A D I R G I Q P V H W G P R S L H R

SEQ. ID. NO. 9 AGTGGATCTGCAACAGATTTCACCTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTATCACT 280  
SEQ. ID. NO. 10 TCACCTAGACGTTGTCTAAAGTGAGACTGGTAGTCGTACACGTCGCACTTCTGGAACGTCTAATAGTGA  
SEQ. ID. NO. 11 S G S A T O F T L T I S S V Q A E D L A D Y H  
SEQ. ID. NO. 12 V D L Q Q I S L P S A V C R L K T L Q I I T  
SEQ. ID. NO. 13 Q W I C N R F H S O H Q Q C A G R P C R L S L

SEQ. ID. NO. 9 GTGGACAGGGTTACAGCTATCCGTACACGTTCCGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGC 350  
SEQ. ID. NO. 10 CACCTGTCCCAATGTGATAGGCATGTGCAAGCCTCCCGCTGGTTCGACCTTTATTTGCCCCGACTACG  
SEQ. ID. NO. 11 C G G G Y S Y P Y T F G G G T K L E I K R A D A  
SEQ. ID. NO. 12 V D R V T A R T R S E G G P S W K N G L M  
SEQ. ID. NO. 13 W T G L Q L S V H V R R G Q Q A G N K T G C

SEQ. ID. NO. 9 TGCACCAACTGTA 363  
SEQ. ID. NO. 10 ACGTGGTTGACAT  
SEQ. ID. NO. 11 A P T V  
SEQ. ID. NO. 12 L H Q L Y  
SEQ. ID. NO. 13 C T N C

FIGURE 10

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

| Seq1(1>107) | Seq2(1>111) | Similarity Index | Gap Number | Gap Length | Consensus Length |
|-------------|-------------|------------------|------------|------------|------------------|
| J591VK.PRO  | MUVKV.PRO   | 60.4             | 2          | 2          | 109              |
| (1>107)     | (1>109)     |                  |            |            |                  |

NIVMTQSPKSMMSVGERVTLTCKAS-ENVVTVVSWYQQKPEQSPKLLIYGASNRYTGVP  
 :I MTQSP.S:S S:G:RVT:TC:AS:::Y::WYQQKP. SPKLLIY AS:.:GVP  
 DIQMTQSPSSLASLGDRVTITCRASODDISNYLNWYQQKPGGSPKLLIYYASRLHSGYP  
 DREFGSGSATQFTLTSSVOAEDLADYHCGGYSY-PYTFGGGTKLEIK  
 RE:GSGS:TD::LT:IS:::ED:A.Y C.QG::P TFGGGTKLEIK  
 SRFSGSGSGTDYSLTYSNLEQED:ATYFCQQGNTLPPTTFGGGTKLEIK

FIGURE 11

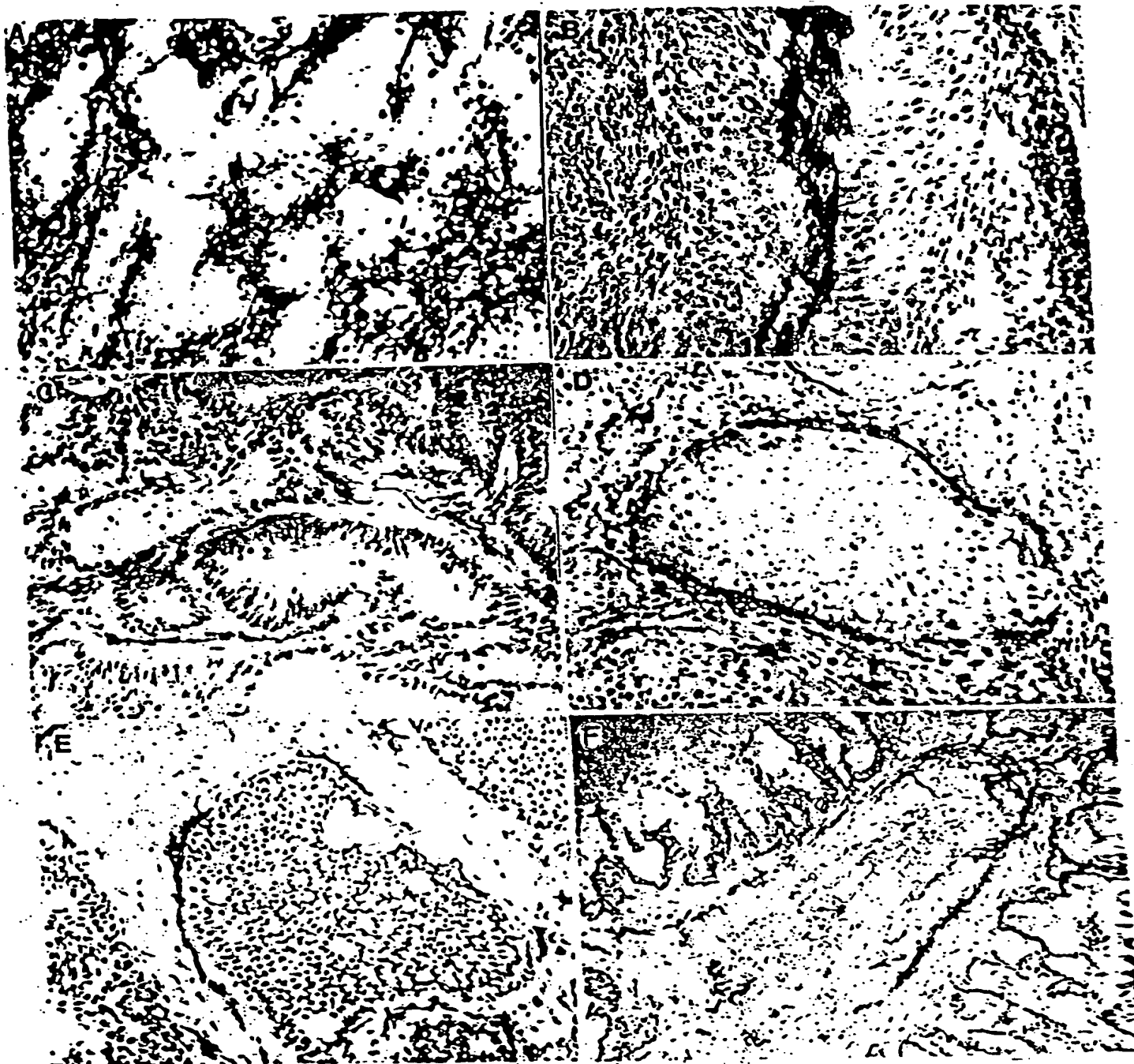


FIGURE 12